



8

SEQUENCE LISTING

<110> Bolton, Alexandra J.
Perez-Casal, Jose
Fontaine, Michael
Potter, Andrew A.

<120> IMMUNIZATION OF DAIRY CATTLE WITH GapC PROTEIN AGAINST
STREPTOCOCCUS INFECTION

<130> 9000-0055

<140> 09/878,781

<141> 2001-06-11

<160> 18

<170> PatentIn Ver. 2.0

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<213> Artificial Sequence

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<212> DNA

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Glu Asn Ile Asp Trp Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala	
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aac ggt gct aaa aaa gtt gtt atc aca gct cct ggt gga aac gac gtt	384
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Arg Gly Gly Asp Leu Arg Arg Ala Arg Ala Gly Ala Ala Asn Ile Val	
195 200 205	
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Asp Glu Ile Asn Ala Ala Met Lys Ala Ala Ser Asn Asp Ser Phe Gly			
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gca ttc cgt cgc atc caa aac gta gaa ggt gtt gaa gtt act cgt atc	96
Ala Phe Arg Arg Ile Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile	
20 25 30	
aac gac ctt aca gat cca aac atg ctt gca cac ttg ttg aaa tat gac	144
Asn Asp Leu Thr Asp Pro Asn Met Leu Ala His Leu Leu Lys Tyr Asp	
35 40 45	
aca act caa ggt cgt ttc gac ggt act gtt gaa gtt aaa gaa ggt gga	192
Thr Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Glu Gly Gly	
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ttc gaa gtt aac ggt caa ttt gtt aaa gtt tct gct gaa cgc gaa cca	240
Phe Glu Val Asn Gly Gln Phe Val Lys Val Ser Ala Glu Arg Glu Pro	
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gca aac att gac tgg gct act gat ggc gta gaa atc gtt ctt gaa gca	288
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Arg Gly Gly Asp Leu Arg Arg Ala Arg Ala Gly Ala Ala Asn Ile Val	
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Gly Ser Leu Phe Asp Ala Thr Gln Thr Lys Val Gln Thr Val Asp Gly	
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Phe Glu Val Asn Gly Asn Phe Ile Lys Val Ser Ala Glu Lys Asp Pro	
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Glu Asn Ile Asp Trp Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala	
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Thr Gly Phe Phe Ala Lys Lys Ala Ala Ala Glu Lys His Leu His Ala	
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145 150 155 160	
gct aaa gct ttg caa gat aac ttt ggt gtt aaa caa ggt ttg atg aca	528
Ala Lys Ala Leu Gln Asp Asn Phe Gly Val Lys Gln Gly Leu Met Thr	
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cct aac tca act ggt gct gct aaa gca atc ggt ctt gta atc cca gaa	672
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Glu Glu Ile Asn Ala Ala Met Lys Ala Ala Ala Asn Asp Ser Tyr Gly	
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Tyr Thr Glu Asp Pro Ile Val Ser Ser Asp Ile Ile Gly Met Ala Tyr	
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ggt tca ttg ttt gat gct act caa act aaa gta caa act gtt gat gga	912
Gly Ser Leu Phe Asp Ala Thr Gln Thr Lys Val Gln Thr Val Asp Gly	
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Asn Gln Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr	
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act gca caa ctt gtt cgT act ctt gag tac ttt gca aaa atc gct aaa	1008
Thr Ala Gln Leu Val Arg Thr Leu Glu Tyr Phe Ala Lys Ile Ala Lys	
325 330 335	
taa	1011

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<212> PRT

<213> Streptococcus uberis

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aca atc cac gct tac act ggt gat caa atg ctt ctt gat gga cct cac	576			
Thr Ile His Ala Tyr Thr Gly Asp Gln Met Leu Leu Asp Gly Pro His				
180 185 190				
cgt ggt ggt gac tta cgt cgt gcc cgt gct ggt gct aac aat att gtt	624			
Arg Gly Gly Asp Leu Arg Arg Ala Arg Ala Gly Ala Asn Asn Ile Val				
195 200 205				
cct aac tca act ggt gct gct aaa gca atc ggt ctt gtt atc cct gaa	672			
Pro Asn Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro Glu				
210 215 220				
tta aat ggt aaa ctt gac ggt gct gca caa cgt gta cca gtt cca aca	720			
Leu Asn Gly Lys Leu Asp Gly Ala Ala Gln Arg Val Pro Val Pro Thr				
225 230 235 240				
ggt tca gta aca gaa tta gta gca gtt ctt aat aaa gaa act tca gta	768			
Gly Ser Val Thr Glu Leu Val Ala Val Leu Asn Lys Glu Thr Ser Val				
245 250 255				
gaa gaa att aac tca gta atg aaa gct gca gct aat gat tca tat ggt	816			
Glu Glu Ile Asn Ser Val Met Lys Ala Ala Ala Asn Asp Ser Tyr Gly				
260 265 270				
tac act gaa gat cca atc gta tca tct gat atc gtt ggt atg tct ttc	864			
Tyr Thr Glu Asp Pro Ile Val Ser Ser Asp Ile Val Gly Met Ser Phe				
275 280 285				
ggt tca tta ttc gat gct act caa act aaa gta caa act gtt gat gga	912			
Gly Ser Leu Phe Asp Ala Thr Gln Thr Lys Val Gln Thr Val Asp Gly				
290 295 300				
aat caa tta gtt aaa gtt gtt tca tgg tat gac aat gaa atg tct tac	960			
Asn Gln Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr				
305 310 315 320				
act gct caa ctt gat cgt aca ctt gag tac ttt gca aaa atc gct aaa	1008			
Thr Ala Gln Leu Asp Arg Thr Leu Glu Tyr Phe Ala Lys Ile Ala Lys				
325 330 335				
taa	1011			

<210> 10
 <211> 336
 <212> PRT
 <213> Streptococcus parauberis

<400> 10

Met	Val	Val	Lys	Val	Gly	Ile	Asn	Gly	Phe	Gly	Arg	Ile	Gly	Arg	Leu
1				5					10					15	
Ala	Phe	Arg	Arg	Ile	Gln	Asn	Val	Glu	Gly	Val	Glu	Val	Thr	Arg	Ile
			20					25					30		
Asn	Asp	Leu	Thr	Asp	Pro	Asn	Met	Leu	Ala	His	Leu	Leu	Lys	Tyr	Asp
		35					40					45			
Thr	Thr	Gln	Gly	Arg	Phe	Asp	Gly	Thr	Val	Glu	Val	Lys	Asp	Gly	Gly
	50					55					60				
Phe	Asp	Val	Asn	Gly	Lys	Phe	Ile	Lys	Val	Ser	Ala	Glu	Lys	Asp	Pro
65					70					75					80
Glu	Gln	Ile	Asp	Trp	Ala	Thr	Asp	Gly	Val	Glu	Ile	Val	Leu	Glu	Ala
			85						90					95	
Thr	Gly	Phe	Phe	Ala	Lys	Lys	Ala	Ala	Ala	Glu	Lys	His	Leu	His	Glu
			100					105					110		
Asn	Gly	Ala	Lys	Lys	Val	Val	Ile	Thr	Ala	Pro	Gly	Gly	Asp	Asp	Val
		115					120					125			
Lys	Thr	Val	Val	Phe	Asn	Thr	Asn	His	Asp	Ile	Leu	Asp	Gly	Thr	Glu
	130					135					140				
Thr	Val	Ile	Ser	Gly	Ala	Ser	Cys	Thr	Thr	Asn	Cys	Leu	Ala	Pro	Met
145					150					155				160	
Ala	Lys	Ala	Leu	Gln	Asp	Asn	Phe	Gly	Val	Lys	Gln	Gly	Leu	Met	Thr
			165						170					175	
Thr	Ile	His	Ala	Tyr	Thr	Gly	Asp	Gln	Met	Leu	Leu	Asp	Gly	Pro	His
		180						185					190		
Arg	Gly	Gly	Asp	Leu	Arg	Arg	Ala	Arg	Ala	Gly	Ala	Asn	Asn	Ile	Val
		195					200					205			
Pro	Asn	Ser	Thr	Gly	Ala	Ala	Lys	Ala	Ile	Gly	Leu	Val	Ile	Pro	Glu
	210					215					220				
Leu	Asn	Gly	Lys	Leu	Asp	Gly	Ala	Ala	Gln	Arg	Val	Pro	Val	Pro	Thr
225					230					235				240	
Gly	Ser	Val	Thr	Glu	Leu	Val	Ala	Val	Leu	Asn	Lys	Glu	Thr	Ser	Val
			245						250					255	
Glu	Glu	Ile	Asn	Ser	Val	Met	Lys	Ala	Ala	Ala	Asn	Asp	Ser	Tyr	Gly
		260						265				270			
Tyr	Thr	Glu	Asp	Pro	Ile	Val	Ser	Ser	Asp	Ile	Val	Gly	Met	Ser	Phe
		275					280					285			

Gly Ser Leu Phe Asp Ala Thr Gln Thr Lys Val Gln Thr Val Asp Gly
 290 295 300
 Asn Gln Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr
 305 310 315 320
 Thr Ala Gln Leu Asp Arg Thr Leu Glu Tyr Phe Ala Lys Ile Ala Lys
 325 330 335

<210> 11
 <211> 1011
 <212> DNA
 <213> Streptococcus iniae

<220>
 <221> CDS
 <222> (1)..(1011)

<400> 11
 atg gta gtt aaa gtt ggt att aac ggt ttc gga cgt atc ggt cgt ctt 48
 Met Val Val Lys Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Leu
 1 5 10 15
 gca ttc cgt cgt att caa aat gtt gaa ggt gtt gaa gta act cgt atc 96
 Ala Phe Arg Arg Ile Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile
 20 25 30
 aat gac ctt aca gat cct aac atg ctt gca cac ttg ttg aaa tat gat 144
 Asn Asp Leu Thr Asp Pro Asn Met Leu Ala His Leu Leu Lys Tyr Asp
 35 40 45
 aca act caa ggt cgt ttt gac ggt aca gtt gaa gtt aaa gat ggt gga 192
 Thr Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Asp Gly Gly
 50 55 60
 ttc gaa gtt aac gga agc ttt gtt aaa gtt tct gca gaa cgc gaa cca 240
 Phe Glu Val Asn Gly Ser Phe Val Lys Val Ser Ala Glu Arg Glu Pro
 65 70 75 80
 gca aac att gac tgg gct act gat ggt gta gac atc gtt ctt gaa gca 288
 Ala Asn Ile Asp Trp Ala Thr Asp Gly Val Asp Ile Val Leu Glu Ala
 85 90 95
 aca ggt ttc ttc gct tct aaa gca gct gct gaa caa cac att cac gct 336
 Thr Gly Phe Phe Ala Ser Lys Ala Ala Ala Glu Gln His Ile His Ala
 100 105 110
 aac ggt gcg aaa aaa gtt gtt atc aca gct cct ggt gga aat gac gtt 384
 Asn Gly Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asn Asp Val
 115 120 125
 aaa aca gtt gtt tac aac act aac cat gat att ctt gat gga act gaa 432
 Lys Thr Val Val Tyr Asn Thr Asn His Asp Ile Leu Asp Gly Thr Glu

130	135	140	
aca gtt atc tca ggt gct tca tgt act	aca aac tgt tta gct cca atg	480	
Thr Val Ile Ser Gly Ala Ser Cys Thr	Thr Asn Cys Leu Ala Pro Met		
145	150 155 160		
gct aaa gca tta caa gat aac ttt ggt gta aaa caa ggt tta atg act	528		
Ala Lys Ala Leu Gln Asp Asn Phe Gly Val Lys Gln Gly Leu Met Thr			
165 170 175			
act atc cat ggt tac act ggt gac caa atg gtt ctt gac gga cca cac	576		
Thr Ile His Gly Tyr Thr Gly Asp Gln Met Val Leu Asp Gly Pro His			
180 185 190			
cgt ggt ggt gat ctt cgt cgt gct cgt gca gct gca gca aac atc gtt	624		
Arg Gly Gly Asp Leu Arg Arg Ala Arg Ala Ala Ala Asn Ile Val			
195 200 205			
cct aac tca act ggt gct gct aaa gca atc ggt ctt gtt atc cca gaa	672		
Pro Asn Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro Glu			
210 215 220			
tta aat ggt aaa ctt gac ggt gct gca caa cgt gtt cct gtt cca act	720		
Leu Asn Gly Lys Leu Asp Gly Ala Ala Gln Arg Val Pro Val Pro Thr			
225 230 235 240			
gga tca gta act gaa tta gta gca gtt ctt gaa aaa gat act tca gta	768		
Gly Ser Val Thr Glu Leu Val Ala Val Leu Glu Lys Asp Thr Ser Val			
245 250 255			
gaa gaa atc aat gca gct atg aaa gca gca gct aac gat tca tac ggt	816		
Glu Glu Ile Asn Ala Ala Met Lys Ala Ala Ala Asn Asp Ser Tyr Gly			
260 265 270			
tac act gaa gat gct atc gta tca tca gat atc gta ggt att tct tac	864		
Tyr Thr Glu Asp Ala Ile Val Ser Ser Asp Ile Val Gly Ile Ser Tyr			
275 280 285			
ggt tca tta ttt gat gct act caa act aaa gta caa act gtt gat gga	912		
Gly Ser Leu Phe Asp Ala Thr Gln Thr Lys Val Gln Thr Val Asp Gly			
290 295 300			
aat caa ttg gtt aaa gtt gtt tca tgg tat gac aat gaa atg tct tac	960		
Asn Gln Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr			
305 310 315 320			
act gct caa ctt gtt cgt act ctt gag tac ttt gca aaa atc gct aaa	1008		
Thr Ala Gln Leu Val Arg Thr Leu Glu Tyr Phe Ala Lys Ile Ala Lys			
325 330 335			
taa	1011		

<210> 12
 <211> 336
 <212> PRT
 <213> Streptococcus iniae

<400> 12
 Met Val Val Lys Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Leu
 1 5 10 15
 Ala Phe Arg Arg Ile Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile
 20 25 30
 Asn Asp Leu Thr Asp Pro Asn Met Leu Ala His Leu Leu Lys Tyr Asp
 35 40 45
 Thr Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Asp Gly Gly
 50 55 60
 Phe Glu Val Asn Gly Ser Phe Val Lys Val Ser Ala Glu Arg Glu Pro
 65 70 75 80
 Ala Asn Ile Asp Trp Ala Thr Asp Gly Val Asp Ile Val Leu Glu Ala
 85 90 95
 Thr Gly Phe Phe Ala Ser Lys Ala Ala Ala Glu Gln His Ile His Ala
 100 105 110
 Asn Gly Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asn Asp Val
 115 120 125
 Lys Thr Val Val Tyr Asn Thr Asn His Asp Ile Leu Asp Gly Thr Glu
 130 135 140
 Thr Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met
 145 150 155 160
 Ala Lys Ala Leu Gln Asp Asn Phe Gly Val Lys Gln Gly Leu Met Thr
 165 170 175
 Thr Ile His Gly Tyr Thr Gly Asp Gln Met Val Leu Asp Gly Pro His
 180 185 190
 Arg Gly Gly Asp Leu Arg Arg Ala Arg Ala Ala Ala Asn Ile Val
 195 200 205
 Pro Asn Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro Glu
 210 215 220
 Leu Asn Gly Lys Leu Asp Gly Ala Ala Gln Arg Val Pro Val Pro Thr
 225 230 235 240
 Gly Ser Val Thr Glu Leu Val Ala Val Leu Glu Lys Asp Thr Ser Val
 245 250 255

Glu Glu Ile Asn Ala Ala Met Lys Ala Ala Ala Asn Asp Ser Tyr Gly
 260 265 270
 Tyr Thr Glu Asp Ala Ile Val Ser Ser Asp Ile Val Gly Ile Ser Tyr
 275 280 285
 Gly Ser Leu Phe Asp Ala Thr Gln Thr Lys Val Gln Thr Val Asp Gly
 290 295 300
 Asn Gln Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr
 305 310 315 320
 Thr Ala Gln Leu Val Arg Thr Leu Glu Tyr Phe Ala Lys Ile Ala Lys
 325 330 335

<210> 13
 <211> 961
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: SpyGapC

<400> 13
 atggttagtta aagttggtat taacggtttc ggtcgtatcg gacgtcttgc accttacaga 60
 tccaaatatg cttgcacact tgttgaaata cgatacaact caaggacgtt ttgatggaac 120
 agttgaagtt aaagaagggt gatttgaagt aaacggaaac ttcatacaag tttctgctga 180
 acgtgatcca gaaaacatcg actgggcaac tgatgggggt gaaatcggtc tggaagcaac 240
 tggtttcttt gctaaaaaag aagcagctga aaaacactta catgctaacg gtgctaaaaa 300
 agttgttatc acagctcctg gtggaaacga tgtaaaaaca gttgttttca aactaacca 360
 cgacattctt gacggtactg aaacagttat ctcaggtgct tcatgtacta caaactgttt 420
 agtccttatg gctaaagtc ttcacgatgc attcgggtatc caaaaagggtc ttatgactac 480
 aatccacgct tatactgggt accaaatgat ccttgacgga ccacaccgtg gtggtgacct 540
 tcgtcgtgca cgcgctgggt ctgcaaacat tgttcctaac tcaactgggt ctgctaaagc 600
 tatcgggtctt gttatcccag aacttaacgg taaacttgat ggtgctgcac aacgtgttcc 660
 tgttccaact ggatcagtaa ctgagttggt tgtaactctt gacaaaaacg tttctgttga 720
 cgaaatcaac tctgctatga aagctgcttc aaacgacagc ttcggttaca ctgaagatcc 780
 aattgtttct tcagatatcg taggcgtatc atacggttca ttgtttgacg caactcaaac 840
 taaagtaatg gaagttgacg gatcacaatt gggttaaagt gtatcatggt atgacaacga 900
 aatgtcttac actgctcaac ttgtacgtac tcttgagtat ttcgcaaaaa ttgctaaata 960
 a 961

<210> 14
 <211> 335
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: SpyGapC
 protein

<400> 14
 Met Val Val Lys Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Leu

1		5		10		15									
Ala	Phe	Arg	Arg	Ile	Gln	Asn	Ile	Glu	Gly	Val	Glu	Val	Thr	Arg	Ile
		20						25					30		
Asn	Asp	Leu	Thr	Asp	Pro	Asn	Met	Leu	Ala	His	Leu	Leu	Lys	Tyr	Asp
		35					40					45			
Thr	Thr	Gln	Gly	Arg	Phe	Asp	Gly	Thr	Val	Glu	Val	Lys	Glu	Gly	Gly
	50					55					60				
Phe	Glu	Val	Asn	Gly	Asn	Phe	Ile	Lys	Val	Ser	Ala	Glu	Arg	Asp	Pro
65					70					75					80
Glu	Ile	Asp	Trp	Ala	Thr	Asp	Gly	Val	Glu	Ile	Val	Leu	Glu	Ala	Thr
				85					90					95	
Ser	Phe	Phe	Ala	Lys	Lys	Glu	Ala	Ala	Glu	Lys	His	Leu	His	Ala	Asn
			100					105					110		
Gly	Ala	Lys	Lys	Val	Val	Ile	Thr	Ala	Pro	Gly	Gly	Asn	Asp	Val	Lys
	115						120					125			
Thr	Val	Val	Phe	Asn	Thr	Asn	His	Asp	Ile	Leu	Asp	Gly	Thr	Glu	Thr
	130					135					140				
Val	Ile	Ser	Gly	Ala	Ser	Cys	Thr	Thr	Asn	Cys	Leu	Ala	Pro	Met	Ala
145					150					155					160
Lys	Ala	Leu	His	Asp	Ala	Phe	Gly	Ile	Gln	Lys	Gly	Leu	Met	Thr	Thr
				165					170					175	
Ile	His	Ala	Tyr	Thr	Gly	Asp	Gln	Met	Ile	Leu	Asp	Gly	Pro	His	Arg
		180						185					190		
Gly	Gly	Asp	Leu	Arg	Arg	Ala	Arg	Ala	Gly	Ala	Ala	Asn	Ile	Val	Pro
	195						200					205			
Asn	Ser	Thr	Gly	Ala	Ala	Lys	Ala	Ile	Gly	Leu	Val	Ile	Pro	Glu	Leu
	210					215					220				
Asn	Gly	Lys	Leu	Asp	Gly	Ala	Ala	Gln	Arg	Val	Pro	Val	Pro	Thr	Gly
225					230					235					240
Ser	Val	Thr	Glu	Leu	Val	Val	Thr	Leu	Asp	Lys	Asn	Val	Ser	Val	Asp
			245						250					255	
Glu	Ile	Asn	Ser	Ala	Met	Lys	Ala	Ala	Ser	Asn	Asp	Ser	Phe	Gly	Tyr
		260						265					270		
Thr	Glu	Asp	Pro	Ile	Val	Ser	Ser	Asp	Ile	Val	Gly	Val	Ser	Tyr	Gly
	275						280					285			
Ser	Leu	Phe	Asp	Ala	Thr	Gln	Thr	Lys	Val	Met	Glu	Val	Asp	Gly	Ser

290 295 300

Gln Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr Thr
 305 310 315 320

Ala Gln Leu Val Arg Thr Leu Glu Tyr Phe Ala Lys Ile Ala Lys
 325 330 335

<210> 15
 <211> 1010
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: SeqGapC

<400> 15
 atggtagtta aagttggtat taacggtttc ggtcgtatcg gacgtcttgc attccgctcg 60
 attcaaaatg ttgaagggtg tgaagtaact cgtatcaacg accttacaga tccaaacatg 120
 cttgcacact tggtgaaata cgatacaact caaggacgtt ttgacggaac tggtgaagtt 180
 aaagaagggtg gatttgaagt aaacggaaac ttcacaaag tttctgctga acgtgatcca 240
 gaaaacatcg actgggcaac tgacggtggt gaaatcgttc tggaagcaac tggtttcttt 300
 gctaaaaaag aagctgctga aaaaccctta catgctaacg gtgctaaaaa agttggtatc 360
 acagctcctg gtggaaacga cgtaaacag ttgttttcaa cactaaccac gacattcttg 420
 acggtactga aacagttatc tcaggtgctt catgtactac aaactgttta gctcctatgg 480
 ctaaagctct tcacgatgca tttggtatcc aaaaaggctt tatgactaca atccacgctt 540
 atactggtga ccaaatgatc gttgatggac accgtggtgg tggatgattc cgtcgtgctc 600
 gtgctggtgc tgcaaacatt gttcctaact caactggtgc tcgtaaagct atcgggtcttg 660
 ttatcccaga attgaacggt aaacttgatg gtgctgcaca acgtgttcct gttccaactg 720
 gatcagtaac tgagttggtt gtaactcttg acaaaaacgt ttctgttgac gaaatcaacg 780
 ctgctatgaa agctgcttca aacgacagct tcggttacac tgaagatcca attgtttctt 840
 cagatatcgt aggcgtatca tacggttcat tgtttgacgc aactcaaact aaagttatgg 900
 aagttgatgg atcacaattg gttaaagttg tatcatggta tgacaacgaa atgtcttaca 960
 ctgctcaact tgttcgtaca cttgagtatt ttgcaaaaat cgctaaataa 1010

<210> 16
 <211> 336
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: SeqGapC
 protein

<400> 16
 Met Val Val Lys Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Leu
 1 5 10 15

Ala Phe Arg Arg Ile Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile
 20 25 30

Asn Asp Leu Thr Asp Pro Asn Met Leu Ala His Leu Leu Lys Tyr Asp
 35 40 45

Thr Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Glu Gly Gly
50 55 60

Phe Glu Val Asn Gly Asn Phe Ile Lys Val Ser Ala Glu Arg Asp Pro
65 70 75 80

Glu Asn Ile Asp Trp Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala
85 90 95

Thr Ser Phe Phe Ala Lys Lys Glu Ala Ala Glu Lys Pro Leu His Ala
100 105 110

Asn Gly Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asn Asp Val
115 120 125

Lys Gln Leu Phe Ser Thr Leu Thr Thr Ser Ile Leu Asp Gly Thr Glu
130 135 140

Thr Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met
145 150 155 160

Ala Lys Ala Leu His Asp Ala Phe Gly Ile Gln Lys Gly Leu Met Thr
165 170 175

Thr Ile His Ala Tyr Thr Gly Asp Gln Met Ile Val Asp Gly His Arg
180 185 190

Gly Gly Gly Asp Leu Arg Arg Ala Arg Ala Gly Ala Ala Asn Ile Val
195 200 205

Pro Asn Ser Thr Gly Ala Arg Lys Ala Ile Gly Leu Val Ile Pro Glu
210 215 220

Leu Asn Gly Lys Leu Asp Gly Ala Ala Gln Arg Val Pro Val Pro Thr
225 230 235 240

Gly Ser Val Thr Glu Leu Val Val Thr Leu Asp Lys Asn Val Ser Val
245 250 255

Asp Glu Ile Asn Ala Ala Met Lys Ala Ala Ser Asn Asp Ser Thr Gly
260 265 270

171	111	Glu	Asp	Pro	Pro	Val	Ser	Ser	Asp	Pro	Val	Ser	Val	Ser	171
		275					280					285			

290	295	300
-----	-----	-----

305 310 315 320

325	330	335
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<210> 17
 <211> 933
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: BovGapC

<400> 17
 cgcatcgggc gcctgggtcac cagggctgct ttttaattctg gcaaagtgga catcgtcgcc 60
 atcaatgacc ctttcattga ctttcactac atgggtctaca tgttccagta tgattccacc 120
 cacggcaagt tcaacggcac agtcaaggca gagaacggga agctcgtcac caatggaaaag 180
 gccatcacca tcttcaggga gcgagatcct gccaacatca agtgggggtga tgctgggtgct 240
 gagtatgtag tggagtccac tgggggtcttc actaccatgg agaaggctgg ggctcacttg 300
 aagggtggcg ccaagagggg catcatctct gcaccttctg ccgatgcccc catgtttgtg 360
 atgggctgta accacgaaag tataacaaca ccctcaagat tgtcagcaat gcctcctgca 420
 ccaccaactg cttggccccc ctggccaagg tcatccatga cccatttggc atcgtggagg 480
 gacttatgac cactgtccac gccattactg ccaccagaa gactgtggat ggccccctcg 540
 ggaagctgtg gcgtgacggc cgaggggctg ccagaatat tatccctgct tctactggcg 600
 ctgccaaggc cgtgggcaag gtcattcctg agctcaacgg gaagctcact ggcatggcct 660
 tccgcgtccc cactcccaac gtgtctgttg tggatctgac ctgccgcctg gagaaacctg 720
 ccaagtatga tgagatcaag aagggtggtga agcaggcgrc agagggccgt ctcaagggca 780
 ttctaggcta cactgaggac caggttgtct cctgcgactt caacagcgat actcactctt 840
 ccaccttcga tgctggggct ggcgtagccc tcaacgccc ctttgtcaag ctcatatcct 900
 ggtacgacaa tgaatttggc tacagcaaac agg 933

<210> 18
 <211> 311
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: BovGapC
 protein

<400> 18
 Arg Ile Gly Arg Leu Val Thr Arg Ala Ala Phe Asn Ser Gly Lys Val
 1 5 10 15
 Asp Ile Val Ala Ile Asn Asp Pro Phe Ile Asp Leu His Tyr Met Val
 20 25 30
 Tyr Met Phe Gln Tyr Asp Ser Thr His Gly Lys Phe Asn Gly Thr Val
 35 40 45
 Lys Ala Glu Asn Gly Lys Leu Val Ile Asn Gly Lys Ala Ile Thr Ile
 50 55 60
 Phe Gln Glu Arg Asp Pro Ala Asn Ile Lys Trp Gly Asp Ala Gly Ala
 65 70 75 80

Glu	Tyr	Val	Val	Glu	Ser	Thr	Ser	Val	Phe	Thr	Thr	Met	Glu	Lys	Ala	85	90	95	
Gly	Ala	His	Leu	Lys	Gly	Gly	Ala	Lys	Arg	Val	Ile	Ile	Ser	Ala	Pro	100	105	110	
Ser	Ala	Asp	Ala	Pro	Met	Phe	Val	Met	Gly	Val	Asn	His	Glu	Lys	Tyr	115	120	125	
Asn	Asn	Thr	Leu	Lys	Ile	Val	Ser	Asn	Ala	Ser	Cys	Thr	Thr	Asn	Cys	130	135	140	
Leu	Ala	Pro	Leu	Ala	Lys	Val	Ile	His	Asp	His	Phe	Gly	Ile	Val	Glu	145	150	155	160
Gly	Leu	Met	Thr	Thr	Val	His	Ala	Ile	Thr	Ala	Thr	Gln	Lys	Thr	Val	165	170	175	
Asp	Gly	Pro	Ser	Gly	Lys	Leu	Trp	Arg	Asp	Gly	Arg	Gly	Ala	Ala	Gln	180	185	190	
Asn	Ile	Ile	Pro	Ala	Ser	Thr	Gly	Ala	Ala	Lys	Ala	Val	Gly	Lys	Val	195	200	205	
Ile	Pro	Glu	Leu	Asn	Gly	Lys	Leu	Thr	Gly	Met	Ala	Phe	Arg	Val	Pro	210	215	220	
Thr	Pro	Asn	Val	Ser	Val	Val	Asp	Leu	Thr	Cys	Arg	Leu	Glu	Lys	Pro	225	230	235	240
Ala	Lys	Tyr	Asp	Glu	Ile	Lys	Lys	Val	Val	Lys	Gln	Ala	Ser	Glu	Gly	245	250	255	
Pro	Leu	Lys	Gly	Ile	Leu	Gly	Tyr	Thr	Glu	Asp	Gln	Val	Val	Ser	Cys	260	265	270	
Asp	Phe	Asn	Ser	Asp	Thr	His	Ser	Ser	Thr	Phe	Asp	Ala	Gly	Ala	Gly	275	280	285	
Ile	Ala	Leu	Asn	Asp	His	Phe	Val	Lys	Leu	Ile	Ser	Trp	Tyr	Asp	Asn	290	295	300	
Glu	Phe	Gly	Tyr	Ser	Lys	Gln										305	310		